

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/274,752C

DATE: 03/13/2001
TIME: 17:08:17

Input Set : A:\A-67501.app
Output Set: N:\CRF3\03132001\I274752C.raw

re-run
p.5

3 <110> APPLICANT: Goetzl, Edward L.
4 An, Songzhu
6 <120> TITLE OF INVENTION: Human Polypeptide Receptors for Lysophospholipids and
7 Sphingolipids and Nucleic Acids Encoding the Same
9 <130> FILE REFERENCE: A-67501/DJB/TAL
11 <140> CURRENT APPLICATION NUMBER: 09/274,752C
12 <141> CURRENT FILING DATE: 1999-03-23
14 <160> NUMBER OF SEQ ID NOS: 29
16 <170> SOFTWARE: PatentIn Ver. 2.0
18 <210> SEQ ID NO: 1
19 <211> LENGTH: 382
20 <212> TYPE: PRT
21 <213> ORGANISM: Homo sapiens
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27 Tyr Asn Asn Ser Gly Lys Glu Leu Ser Ser His Trp Arg Pro Lys Asp
28 20 25 30
30 Val Val Val Val Ala Leu Gly Leu Thr Val Ser Val Leu Val Leu Leu
31 35 40 45
33 Thr Asn Leu Leu Val Ile Ala Ala Ile Ala Ser Asn Arg Arg Phe His
34 50 55 60
36 Gln Pro Ile Tyr Tyr Leu Leu Gly Asn Leu Ala Ala Ala Asp Leu Phe
37 65 70 75 80
39 Ala Gly Val Ala Tyr Leu Phe Leu Met Phe His Thr Gly Pro Arg Thr
40 85 90 95
42 Ala Arg Leu Ser Leu Glu Gly Trp Phe Leu Arg Gln Gly Leu Leu Asp
43 100 105 110
45 Thr Ser Leu Thr Ala Ser Val Ala Thr Leu Leu Ala Ile Ala Val Glu
46 115 120 125
48 Arg His Arg Ser Val Met Ala Val Gln Leu His Ser Arg Leu Pro Arg
49 130 135 140
51 Gly Arg Val Val Met Leu Ile Val Gly Val Trp Val Ala Ala Leu Gly
52 145 150 155 160
54 Leu Gly Leu Leu Pro Ala His Ser Trp His Cys Leu Cys Ala Leu Asp
55 165 170 175
57 Arg Cys Ser Arg Met Ala Pro Leu Leu Ser Arg Ser Tyr Leu Ala Val
58 180 185 190
60 Trp Ala Leu Ser Ser Leu Leu Val Phe Leu Leu Met Val Ala Val Tyr
61 195 200 205
63 Thr Arg Ile Phe Phe Tyr Val Arg Arg Arg Val Gln Arg Met Ala Glu
64 210 215 220
66 His Val Ser Cys His Pro Arg Tyr Arg Glu Thr Thr Leu Ser Leu Val
67 225 230 235 240
69 Lys Thr Val Val Ile Ile Leu Gly Ala Phe Val Val Cys Trp Thr Pro
70 245 250 255
72 Gly Gln Val Val Leu Leu Leu Asp Gly Leu Gly Cys Glu Ser Cys Asn

**Does Not Comply
Corrected Diskette Needed**

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73          260          265          270
75 Val Leu Ala Val Glu Lys Tyr Phe Leu Leu Leu Ala Glu Ala Asn Ser
76          275          280          285
78 Leu Val Asn Ala Ala Val Tyr Ser Cys Arg Asp Ser Glu Met Arg Arg
79          290          295          300
81 Thr Phe Arg Arg Leu Leu Cys Cys Ala Cys Leu Arg Gln Ser Thr Arg
82 305          310          315          320
84 Glu Ser Val His Tyr Thr Ser Ser Ala Gln Gly Gly Ala Ser Thr Arg
85          325          330          335
87 Ile Met Leu Pro Glu Asn Gly His Pro Leu Met Thr Pro Pro Phe Ser
88          340          345          350
90 Tyr Leu Glu Leu Gln Arg Tyr Ala Ala Ser Asn Lys Ser Thr Ala Pro
91          355          360          365
93 Asp Asp Leu Trp Val Leu Leu Ala Gln Pro Asn Gln Gln Asp
94          370          375          380
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98 <211> LENGTH: 1734
99 <212> TYPE: DNA
100 <213> ORGANISM: Homo sapiens
102 <400> SEQUENCE: 2
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105 atcggtctct tctataacaa cagtggcaaa gagctcagct cccactggcg gcccaaggat 180
106 gtggctcggtg tggcactggg gctgaccgtc agcgtgctgg tgctgctgac caatctgctg 240
107 gtcatagcag ccacgcctc caaccgccgc ttccaccagc ccactacta cctgctcggc 300
108 aatctggccg cggtgacct cttcgcgggc gtggcctacc tcttctcat gttccacact 360
109 ggtccccgca cagccccgact ttcaactgag ggctgggtcc tgcggcaggg cttgctggac 420
110 acaagcctca ctgcgtcggt ggccacactg ctggccatcg ccgtggagct gcaccgcagt 480
111 gtgatgtccg tgcagctgca cagccgcctg ccccgctggc gcgtggctat gctcattgtg 540
112 ggcgtgtggg tggctgccct gggcctgggg ctgctgcctg cccactcctg gactgcctc 600
113 tgtgccctgg accgctgctc acgcatggca cccctgctca gccgtccta ttggccgctc 660
114 tgggctctgt cgagcctgtc tgtcttctct ctcatgggtg ctgtgtacac ccgcattttc 720
115 ttctacgtgc ggcggcgagt gcagcgcctg gcagagcatg tcagctgcca ccccgctac 780
116 cgagagacca cgctcagcct ggtcaagact gttgtcatca tcctgggggc gttcgtggtc 840
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121 gccagcactc gcacatgctt tcccagaaac ggccaccac tgatgactcc acccttttagc 1140
122 taccttgaac ttacagcgta cgcggcaagc aacaaatcca cagccctga tgacttgggtg 1200
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128 gctctctcgg gccatgctac ccggtatgac tgggtaatga ggacagactg tggacacccc 1560
129 atctacctga gctctattct ttacgagcag agactgaggg gtgcagagtg tgagctggga 1620
130 aaggtttgtg gctccttgca gcctccaggg actggcctgt cccaataga attgaagcag 1680
131 tccacgggga ggggatgata caaggagtaa acctttcttt aactcaaaa aaaa 1734

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133 <210> SEQ ID NO: 3
134 <211> LENGTH: 353
135 <212> TYPE: PRT
136 <213> ORGANISM: Homo sapiens
138 <400> SEQUENCE: 3
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142 His Tyr Asn Tyr Thr Lys Glu Thr Leu Glu Thr Gln Glu Thr Thr Ser
143           20           25           30
145 Arg Gln Val Ala Ser Ala Gly Ile Val Ile Leu Cys Cys Ala Ile Val
146           35           40           45
148 Val Glu Asn Leu Leu Val Leu Ile Ala Val Ala Arg Asn Ser Lys Phe
149           50           55           60
151 His Ser Ala Met Tyr Leu Phe Leu Gly Asn Leu Ala Ala Ser Asp Leu
152   65           70           75           80
154 Leu Ala Gly Val Ala Phe Val Ala Asn Thr Leu Leu Ser Gly Ser Val
155           85           90           95
157 Thr Leu Arg Leu Thr Pro Val Gln Trp Phe Ala Arg Glu Gly Ser Ala
158           100          105          110
160 Ser Ile Thr Leu Ser Ala Ser Val Gly Ser Leu Leu Ala Ile Ala Ile
161           115          120          125
163 Glu Arg His Val Ala Ile Ala Lys Val Lys Leu Tyr Gly Ser Cys Lys
164           130          135          140
166 Ser Cys Arg Met Leu Leu Leu Ile Gly Ala Ser Trp Leu Ile Ser Leu
167   145          150          155          160
169 Val Leu Gly Gly Leu Pro Ile Leu Gly Trp Asn Cys Leu Gly His Leu
170           165          170          175
172 Glu Ala Cys Ser Thr Val Leu Pro Leu Tyr Ala Lys His Tyr Val Leu
173           180          185          190
175 Cys Val Val Thr Ile Phe Ser Ile Ile Leu Leu Ala Ile Val Ala Leu
176           195          200          205
178 Tyr Val Arg Ile Tyr Cys Val Val Arg Ser Ser His Ala Asp Met Ala
179           210          215          220
181 Ala Pro Gln Thr Leu Ala Leu Leu Lys Thr Val Thr Ile Val Leu Gly
182   225          230          235          240
184 Val Phe Ile Val Cys Trp Leu Pro Ala Phe Ser Ile Leu Leu Leu Asp
185           245          250          255
187 Tyr Ala Cys Pro Val His Ser Cys Pro Ile Leu Tyr Lys Ala His Tyr
188           260          265          270
190 Phe Phe Ala Val Ser Thr Leu Asn Ser Leu Leu Asn Pro Val Ile Tyr
191           275          280          285
193 Thr Trp Arg Ser Arg Asp Leu Arg Arg Glu Val Leu Arg Pro Leu Gln
194           290          295          300
196 Cys Trp Arg Pro Gly Val Gly Val Gln Gly Arg Arg Arg Val Gly Thr
197   305          310          315          320
199 Pro Gly His His Leu Pro Leu Arg Ser Ser Ser Ser Leu Glu Arg
200           325          330          335
202 Gly Met His Met Pro Thr Ser Pro Thr Phe Leu Glu Gly Asn Thr Val
203           340          345          350

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205 Val

209 <210> SEQ ID NO: 4

210 <211> LENGTH: 1122

211 <212> TYPE: DNA

212 <213> ORGANISM: Homo sapiens

214 <400> SEQUENCE: 4

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215 atgggcagct tgtactcgga gtacctgaac cccaacaagg tccaggaaca ctataattat 60
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217 gtcactcctct gttgcgccaat gcaggagacg acctcccgcc aggtggcctc ggccttcac 180
218 gtcactcctct gttgcgccaat tgtggtgaa aaccttcttg tgctcattgc ggtggcccga 240
219 aacagcaagt tccactcggc aatgtacctg tttctgggca acctggccgc ctccgatcta 300
220 ctggcaggcg tggccttcgt agccaatadd ttgctctctg gctctgtcac gctgaggetg 360
221 acgcctgtgc agtggtttgc ccgggagggc tctgcctcca tcacgtctc ggcctctgtc 420
222 ttcagcctcc tggccatcgc cattgagcgc cactgggcca ttgccaagg caagctgtat 480
223 ggcagcgaca agagctgccg catgcttctg ctcatcggg cctcgtggct catctcgctg 540
224 gtccctgggtg gcctgccaat ccttggctgg aactgcctgg gccacctega ggcctgtctc 600
225 actgtcctgc ctctctacgc caagcattat gtgctgtgcg tggtagccat cttctccac 660
226 atcctgtttg ccactcgtgg cctgtacgtg cgcactact gctggtccg ctcaagccac 720
227 gctgacatgg ccgcccgcga gacgtagcc ctgctcaaga cggtcacccat cgtgctaggc 780
228 gtctttatcg tctgctggct gccgccttc agcatcctcc ttctggacta tgcctgtccc 840
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230 tccctgtctc acccgtcat ctacacgtgg cgcagccggg acctgcggcg ggaggtgctt 960
231 cggcgcgtgc agtgcctggc gccgggggtg ggggtgcaag gacggaggcg ggtcgggacc 1020
232 ccgggccacc acctcctgcc actccgcagc tccagctccc tggagagggg catgcacatg 1080
233 cccacgtcac ccacgtttct ggagggcaac acggtggtct ga 1122

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235 <210> SEQ ID NO: 5

236 <211> LENGTH: 375

237 <212> TYPE: DNA

238 <213> ORGANISM: Homo sapiens

240 <400> SEQUENCE: 5

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242 agggccagat ggtcatcatg ggccagtgt actacaacga gaccatcggc ttcttctata 120
243 acaacagtgg caaagagctc agctccact ggcggcccaa ggatgtggtc gtggtggcac 180
244 tggggctgac cgtcagcgtg ctggtgctgc tgaccaatct gctggtcata gcagccatcg 240
245 cctccaaccg ccgcttccac cagcccatct actacctgt cggcaatctg gcgcgggtg 300
246 acctcttcgc gggcgtggct acctcttct catgttccac actggtcccc gcacagccc 360
247 actttcactt gaggg 375

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249 <210> SEQ ID NO: 6

250 <211> LENGTH: 8

251 <212> TYPE: PRT

252 <213> ORGANISM: combination of rat and human.

254 <400> SEQUENCE: 6

255 Leu Leu Ala Ile Ala Ile Glu Arg

256 1 5

259 <210> SEQ ID NO: 7

260 <211> LENGTH: 22

261 <212> TYPE: DNA

262 <213> ORGANISM: combination of rat and human.

264 <220> FEATURE:

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265 <221> NAME/KEY: misc_feature
 266 <222> LOCATION: (6)
 267 <223> OTHER INFORMATION: The n at position 6 can be g or c.
 269 <220> FEATURE:
 270 <221> NAME/KEY: misc_feature
 271 <222> LOCATION: (12)
 272 <223> OTHER INFORMATION: The n at position 12 can be c or t.
 274 <220> FEATURE:
 275 <221> NAME/KEY: misc_feature
 276 <222> LOCATION: (17)
 277 <223> OTHER INFORMATION: The n at position 17 can be c or t.
 279 <220> FEATURE:
 280 <221> NAME/KEY: misc_feature
 281 <222> LOCATION: (21)
 282 <223> OTHER INFORMATION: The n at position 21 can be a or c.
 284 <400> SEQUENCE: 7
 285 ctctngcca tngcatngag ng 22
 287 <210> SEQ ID NO: 8
 288 <211> LENGTH: 8
 289 <212> TYPE: PRT
 290 <213> ORGANISM: combination of rat and human.
 292 <400> SEQUENCE: 8
 293 Leu Leu Leu Leu Asp Ser Thr Cys
 294 1 5
 297 <210> SEQ ID NO: 9
 298 <211> LENGTH: 22
 299 <212> TYPE: DNA
 300 <213> ORGANISM: combination of rat and human.
 302 <220> FEATURE:
 303 <221> NAME/KEY: misc_feature
 304 <222> LOCATION: (4), (15), (21) 15 21
 305 <223> OTHER INFORMATION: The n at position 4, 16, and 22 can be c or g.
 307 <220> FEATURE:
 308 <221> NAME/KEY: misc_feature
 309 <222> LOCATION: (6), (16), (18)
 310 <223> OTHER INFORMATION: The n at position 6 and 8 can be a or c.
 312 <220> FEATURE:
 313 <221> NAME/KEY: misc_feature
 314 <222> LOCATION: (7), (9), (18) 18
 315 <223> OTHER INFORMATION: The n at position 7, 9, and 19 can be a or g.
 317 <400> SEQUENCE: 9
 W--> 318 cagntnnnt ccagnag na 22
 320 <210> SEQ ID NO: 10
 321 <211> LENGTH: 24
 322 <212> TYPE: DNA
 323 <213> ORGANISM: Homo sapiens
 325 <400> SEQUENCE: 10
 326 gcaggacagt ggagcaggcc tcga 24
 328 <210> SEQ ID NO: 11

VERIFICATION SUMMARY

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L:285 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7

L:318 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9